

**Exhibit C**  
**BLAST result of SEQ ID NO:1 versus human genome**

MEGABLAST 1.2.3-Paracel [2001-11-20]

**Reference:**

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),  
"A greedy algorithm for aligning DNA sequences",  
J Comput Biol 2000; 7(1-2):203-14.

Database: Homo\_sapiens.latestgp.masked.fa  
33,840 sequences; 200,810,911,373 total letters

Query= LEX181seqid1  
(1395 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AL133463.16.1.84122	1030	0.0
AL050320.19.1.107057	363	1e-97

>AL133463.16.1.84122  
Length = 84122

Score = 1030 bits (519), Expect = 0.0  
Identities = 519/519 (100%)  
Strand = Plus / Plus

Query: 877 gacacagacagctgtgagcgctggatgagctgcaaaagcgagttcttaaagaagtacatg 936  
|||||  
Sbjct: 28357 gacacagacagctgtgagcgctggatgagctgcaaaagcgagttcttaaagaagtacatg  
28416

Query: 937 cacaaggtgatgaatgacctgccagctgcccctgctcctaccccactgaggtggcctac 996  
|||||  
Sbjct: 28417 cacaaggtgatgaatgacctgccagctgcccctgctcctaccccactgaggtggcctac  
28476

Query: 997 agcacggccgacatcttcgaccgcatcaagcgcaaggacttccgctggaaggacgccagc  
1056  
|||||  
Sbjct: 28477 agcacggccgacatcttcgaccgcatcaagcgcaaggacttccgctggaaggacgccagc  
28536

Query: 1057 gggcccaaggagaagctggagatctacaagcccactgcccggctactgcatccgctccatg  
1116  
|||||  
Sbjct: 28537 gggcccaaggagaagctggagatctacaagcccactgcccggctactgcatccgctccatg  
28596

Query: 1117 ctgtccctggagagcaccacgctggcgccacagcactgctgctacggcgacaacatgcag 1176

Sbjct: 28597 ctgtccctggagagcaccacgctggcgccacagcactgctgctacggcgacaacatgcag 28656

Query: 1177 ctcatcaccaggggcaagggggcgggcacgcccacctcatcagcaccgagttctccgcg 1236

Sbjct: 28657 ctcatcaccaggggcaagggggcgggcacgcccacctcatcagcaccgagttctccgcg 28716

Query: 1237 gagtccactacaaggtggacgtcctgccctggattatctgcaagggtgactggagcagg 1296

Sbjct: 28717 gagtccactacaaggtggacgtcctgccctggattatctgcaagggtgactggagcagg 28776

Query: 1297 tataacgaggcccgccctcccaacaacggacagaagtgacagagagcccctcggacgag 1356

Sbjct: 28777 tataacgaggcccgccctcccaacaacggacagaagtgacagagagcccctcggacgag 28836

Query: 1357 gactacatcaagcagttccaagaggccagggaatattaa 1395

Sbjct: 28837 gactacatcaagcagttccaagaggccagggaatattaa 28875

Score = 528 bits (266), Expect = e-147  
Identities = 267/268 (99%)  
Strand = Plus / Plus

Query: 376 caggtcaccatagaggtggtcgacggtcctgactctgaagcagataaagatcagcatccg 435

Sbjct: 9047 caggtcaccatagaggtggtcgacggtcctgactctgaagcagataaagatcagcatccg 9106

Query: 436 gagaataagcccagctgggtcagtcctccatccccgactggcgggcctgggtggcagaggtcc 495

Sbjct: 9107 gagaataagcccagctgggtcagtcctccatccccgactggcgggcctgggtggcagaggtcc 9166

Query: 496 ctgtccttgccaggggcaaacagcggggaccaggactacragtacgacagtacctcagac 555

Sbjct: 9167 ctgtccttgccaggggcaaacagcggggaccaggactacaagtacgacagtacctcagac 9226

Query: 556 gacagcaacttcctcaacccccccaggggggtgggaccatacagccccaggccaccggact 615

Sbjct: 9227 gacagcaacttcctcaacccccccaggggggtgggaccatacagccccaggccaccggact 9286

Query: 616 tttgaaaccaaagatcagccagaatatg 643  
|||||  
Sbjct: 9287 tttgaaaccaaagatcagccagaatatg 9314

Score = 312 bits (157), Expect = 5e-82  
Identities = 159/161 (98%)  
Strand = Plus / Plus

Query: 220 caccaggctgcacaccaacccttccccagaccgcgattccgacaagagacggggcaccct 279  
|||||  
Sbjct: 1 caccaggctgcacaccaacccttccccagaccgcgattccgacaagagacggggcaccct 60

Query: 280 tcattgcaaagagatttccccagatcctttctccttgatctaccaaactttccagatctt 339  
|||||  
Sbjct: 61 tcattgcaaagagatttccccagatcctttctccttgatctaccaaactttccagatctt 120

Query: 340 tccaaagctgatatcaatgggcagrwttccaaatatccaggt 380  
|||||  
Sbjct: 121 tccaaagctgatatcaatgggcagaaatccaaatatccaggt 161

Score = 290 bits (146), Expect = 2e-75  
Identities = 146/146 (100%)  
Strand = Plus / Plus

Query: 643 gattccacagatggcgaggggtgactggagttctctggtctgtctgcagcgtcacctgcggg 702  
|||||  
Sbjct: 17955 gattccacagatggcgaggggtgactggagttctctggtctgtctgcagcgtcacctgcggg  
18014

Query: 703 aacggcaaccagaaacggaccgggtcttgtggctacgcgtgcactgcaacagaatcgagg 762  
|||||  
Sbjct: 18015 aacggcaaccagaaacggaccgggtcttgtggctacgcgtgcactgcaacagaatcgagg  
18074

Query: 763 acctgtgaccgtccaaactgccagg 788  
|||||  
Sbjct: 18075 acctgtgaccgtccaaactgccagg 18100

Score = 183 bits (92), Expect = 3e-43  
Identities = 92/92 (100%)  
Strand = Plus / Plus

Query: 786 aggaattgaagacacttttaggacagctgccaccgaagtgagtctgcttgcggaagcga 845  
|||||  
Sbjct: 21788 aggaattgaagacacttttaggacagctgccaccgaagtgagtctgcttgcggaagcga  
21847

Query: 846 ggagtttaatgccaccaaactgtttgaagttg 877  
|||||  
Sbjct: 21848 ggagtttaatgccaccaaactgtttgaagttg 21879

>AL050320.19.1.107057  
Length = 107057

Score = 363 bits (183), Expect = 1e-97  
Identities = 183/183 (100%)  
Strand = Plus / Plus

Query: 137 agaataacctcaacgtgggaagtgcaccacatcagaaaccagcttttctctctccaaag  
196  
|||||  
Sbjct: 106875 agaataacctcaacgtgggaagtgcaccacatcagaaaccagcttttctctctccaaag  
106934

Query: 197 aagcaccaagggagcatctggaccaccaggctgcacaccaacccttccccagaccgcat  
256  
|||||  
Sbjct: 106935 aagcaccaagggagcatctggaccaccaggctgcacaccaacccttccccagaccgcat  
106994

Query: 257 tccgacaagagacggggcacccttcattgcaaagagatttccccagatcctttctccttg  
316  
|||||  
Sbjct: 106995 tccgacaagagacggggcacccttcattgcaaagagatttccccagatcctttctccttg  
107054

Query: 317 atc 319  
|||  
Sbjct: 107055 atc 107057

Score = 175 bits (88), Expect = 8e-41  
Identities = 88/88 (100%)  
Strand = Plus / Plus

Query: 51 cacgctgcacatcacctgtctgcgaggctcgggagccgacggggcccgacgcgccgc 110  
|||||  
Sbjct: 58200 cacgctgcacatcacctgtctgcgaggctcgggagccgacggggcccgacgcgccgc  
58259

Query: 111 gggcaacgccagccaagcccagctgcag 138  
|||||  
Sbjct: 58260 gggcaacgccagccaagcccagctgcag 58287